SEQUENCE LISTING

<110> Alitalo, et al.

<120> VEGF-B AND PDGF MODULATION OF STEM CELLS

<130> 28967/39140B

<140> To be assigned
<141> Herewith

<150> US 60/445,021
<151> 2003-02-04

<150> US 60/471,412
<151> 2003-05-16

<160> 30

<170> PatentIn version 3.2

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<212> DNA
<213> Homo sapiens

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gatgtgtata ctcgcgctac ctgccagccc cgggaggtgg tggtgccctt gactgtggag 180

ctcatgggca ccgtggccaa acagctggtg cccagctgcg tgactgtgca gcgctgtggt 240

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cagatcctca tgatccggta cccgagcagt cagctggggg agatgtccct ggaagaacac 360

agccagtgtg aatgcagacc taaaaaaaag gacagtgctg tgaagccaga cagccccagg 420

cccctctgcc cacgctgcac ccagcaccac cagcgccctg acccccggac ctgccgctgc 480

cgctgccgac gccgcagctt cctccgttgc caagggcggg gcttagagct caacccagac 540

acctgcaggt gccggaagct gcgaaggtga 570

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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
-5              -1  1                   5                   10

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
            15                  20                  25

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
        30                  35                  40

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
    45                  50                  55

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
60                  65                  70                  75

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
                80                  85                  90

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
            95                  100                 105

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
        110                 115                 120

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
    125                 130                 135

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
140                 145                 150                 155

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
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gtgtatactc gcgctacctg ccagccccgg gaggtggtgg tgcccttgac tgtggagctc    180

atgggcaccg tggccaaaca gctggtgccc agctgcgtga ctgtgcagcg ctgtggtggc    240

tgctgccctg acgatggcct ggagtgtgtg cccactgggc agcaccaagt ccggatgcag    300

atcctcatga tccggtaccc gagcagtcag ctgggggaga tgtccctgga agaacacagc    360

cagtgtgaat gcagacctaa aaaaaaggac agtgctgtga agccagacag ggctgccact    420
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ccccaccacc gtccccagcc ccgttctgtt ccgggctggg actctgcccc cggagcaccc 480

tccccagctg acatcaccca tcccactcca gccccaggcc cctctgccca cgctgcaccc 540

agcaccacca gcgccctgac ccccggacct gccgccgccg ctgccgacgc cgcagcttcc 600

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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
-5              -1  1               5                   10

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
            15                  20                  25

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
        30                  35                  40

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
    45                  50                  55

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
60                  65                  70                  75

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
                80                  85                  90

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
            95                  100                 105

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
        110                 115                 120

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
    125                 130                 135
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Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
140                 145                 150                 155

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
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Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
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aaattccagt tttccagcaa caaggaacag aacggagtac aagatcctca gcatgagaga 180

attattactg tgtctactaa tggaagtatt cacagcccaa ggtttcctca tacttatcca 240

agaaatacgg tcttggtatg gagattagta gcagtagagg aaaatgtatg gatacaactt 300

acgtttgatg aaagatttgg gcttgaagac ccagaagatg acatatgcaa gtatgatttt 360

gtagaagttg aggaacccag tgatggaact atattagggc gctggtgtgg ttctggtact 420

gtaccaggaa aacagatttc taaaggaaat caaattagga taagatttgt atctgatgaa 480

tattttcctt ctgaaccagg gttctgcatc cactacaaca ttgtcatgcc acaattcaca 540

gaagctgtga gtccttcagt gctacccccc tcagctttgc cactggacct gcttaataat 600

gctataactg cctttagtac cttggaagac cttattcgat atcttgaacc agagagatgg 660

cagttggact tagaagatct atataggcca acttggcaac ttcttggcaa ggcttttgtt 720

tttggaagaa aatccagagt ggtggatctg aaccttctaa cagaggaggt aagattatac 780

agctgcacac ctcgtaactt ctcagtgtcc ataagggaag aactaaagag aaccgatacc 840

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cacaattgca atgaatgtca atgtgtccca agcaaagtta ctaaaaaata ccacgaggtc 960

cttcagttga gaccaaagac cggtgtcagg ggattgcaca aatcactcac cgacgtggcc 1020

ctggagcacc atgaggagtg tgactgtgtg tgcagaggga gcacaggagg atagccgcat 1080

caccaccagc agctcttgcc cagagctgtg cagtgcagtg gctgattcta ttagagaacg 1140

tatgcgttat ctccatcctt aatctcagtt gtttgcttca aggacctttc atcttcagga 1200

tttacagtgc attctgaaag aggagacatc aaacagaatt aggagttgtg caacagctct 1260

tttgagagga ggcctaaagg acaggagaaa aggtcttcaa tcgtggaaag aaaattaaat 1320

gttgtattaa atagatcacc agctagtttc agagttacca tgtacgtatt ccactagctg 1380

ggttctgtat ttcagttctt tcgatacggc ttagggtaat gtcagtacag gaaaaaaact 1440

gtgcaagtga gcacctgatt ccgttgcctt gcttaactct aaagctccat gtcctgggcc 1500

taaaatcgta taaaatctgg attttttttt ttttttttgc tcatattcac atatgtaaac 1560

cagaacattc tatgtactac aaacctggtt tttaaaaagg aactatgttg ctatgaatta 1620

aacttgtgtc rtgctgatag gacagactgg atttttcata tttcttatta aaatttctgc 1680

catttagaag aagagaacta cattcatggt ttggaagaga taaacctgaa aagaagagtg 1740

gccttatctt cactttatcg ataagtcagt ttatttgttt cattgtgtac atttttatat 1800

tctccttttg acattataac tgttggcttt tctaatcttg ttaaatatat ctatttttac 1860

caaaggtatt taatattctt ttttatgaca acttagatca actattttta gcttggtaaa 1920

tttttctaaa cacaattgtt atagccagag gaacaaagat ggatataaaa atattgttgc 1980

cctggacaaa aatacatgta tntccatccc ggaatggtgc tagagttgga ttaaacctgc 2040

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ataattaa 2108

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<212> PRT
<213> Homo sapiens

<400> 7

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Arg Arg Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
            20                  25                  30

Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
        35                  40                  45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
    50                  55                  60

His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
65                  70                  75                  80

Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
                85                  90                  95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
            100                 105                 110

Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
        115                 120                 125

Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
    130                 135                 140

Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                 150                 155                 160
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Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
                165                 170                 175

Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
            180                 185                 190

Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
        195                 200                 205

Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
    210                 215                 220

Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225                 230                 235                 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
                245                 250                 255

Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
            260                 265                 270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
        275                 280                 285

His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
    290                 295                 300

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
305                 310                 315                 320

His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
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Cys Val Cys Arg Gly Ser Thr Gly Gly
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<213> Homo sapiens

<220>
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<222> (176)..(1288)

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ggagcagaac ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg 178

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                                                                  Met
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cac cgg ctc atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc      226
His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser
            5                   10                  15

tgt cgg gac act tct gca acc ccg cag agc gca tcc atc aaa gct ttg      274
Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu
        20                  25                  30

cgc aac gcc aac ctc agg cga gat gag agc aat cac ctc aca gac ttg      322
Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu
    35                  40                  45


tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag      370
Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln
50                  55                  60                  65

agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg      418
Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp
                70                  75                  80

cgg ctt cac tct cag gag aat aca cgg ata cag cta gtg ttt gac aat      466
Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn
            85                  90                  95

cag ttt gga tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt      514
Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe
        100                 105                 110

gtg gaa gtt gaa gat ata tcc gaa acc agt acc att att aga gga cga      562
Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg
    115                 120                 125

tgg tgt gga cac aag gaa gtt cct cca agg ata aaa tca aga acg aac      610
Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn
130                 135                 140                 145

caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct      658
Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro
                150                 155                 160

gga ttc aag att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca      706
Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala
            165                 170                 175

gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg gta      754
Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val
        180                 185                 190

tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat gct      802
Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala
    195                 200                 205

ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag      850
Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys
210                 215                 220                 225

tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg      898
Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu
                230                 235                 240
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gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa      946
Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys
            245                 250                 255

gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc act      994
Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr
        260                 265                 270

ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat     1042
Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn
    275                 280                 285

gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat     1090
Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn
290                 295                 300                 305

tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg     1138
Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly
                310                 315                 320

aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag cct ggc cac     1186
Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His
            325                 330                 335

atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc cag     1234
Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln
        340                 345                 350

ttg gat cac cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct     1282
Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro
    355                 360                 365

cga taa gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg      1338
Arg
370
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agggtgagat aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc   1398

aatgaacaca agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa   1458

aggtatatca tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga   1518

ggttatatat gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa   1578

tgtttttttt ggtatatata accaggtaca ccagagctta catatgtttg agttagactc   1638

ttaaaatcct ttgccaaaat aagggatggt caaatatatg aaacatgtct ttagaaaatt   1698

taggagataa atttattttt aaattttgaa acacaaaaca attttgaatc ttgctctctt   1758

aaagaaagca tcttgtatat taaaaatcaa aagatgaggc tttcttacat atacatctta   1818

gttgattatt aaaaaaggaa aaaggtttcc agagaaaagg ccaataccta agcatttttt   1878

ccatgagaag cactgcatac ttacctatgt ggactgtaat aacctgtctc caaaaccatg   1938

ccataataat ataagtgctt tagaaattaa atcattgtgt tttttatgca ttttgctgag   1998

gcatccttat tcatttaaca cctatctcaa aaacttactt agaaggtttt ttattatagt   2058

cctacaaaag acaatgtata agctgtaaca gaattttgaa ttgtttttct ttgcaaaacc   2118

cctccacaaa agcaaatcct ttcaagaatg gcatgggcat tctgtatgaa cctttccaga   2178
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cgtaactgga aaccg 2253

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<212> PRT
<213> Homo sapiens

<400> 9

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
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20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
35 40 45

Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
50 55 60

Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65 70 75 80

Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
85 90 95

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
100 105 110

Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
115 120 125

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145 150 155 160

Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
165 170 175

Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
180 185 190

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
195 200 205

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Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
    210                 215                 220

Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
225                 230                 235                 240

Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
                245                 250                 255

Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
            260                 265                 270

Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
        275                 280                 285

Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
    290                 295                 300

Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
305                 310                 315                 320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
                325                 330                 335

His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
            340                 345                 350

Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
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Pro Arg
    370
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<213> Artificial sequence

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<223> PDGF-C Core Domain

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Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu
            20                  25                  30
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Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val
        35                  40                  45

Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu
    50                  55                  60

Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu
65                  70                  75                  80

Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr
                85                  90                  95

Asp Val Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly
            100                 105                 110

Ser Thr Gly Gly
        115
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<210> 11
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<212> DNA
<213> Homo sapiens

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<222> (57)..(629)

<400> 11

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aac ttt ctg ctg tct tgg gtg cat tgg agc ctc gcc ttg ctg ctc tac  107
Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu Tyr
              5                  10                  15

ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga gga  155
Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly
         20                  25                  30

ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag cgc  203
Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg
     35                  40                  45

agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag tac  251
Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
 50                  55                  60                  65

cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccc ctg atg  299
Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
                 70                  75                  80

cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc act  347
Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr
             85                  90                  95
```

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gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac caa   395
Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
        100                 105                 110

ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt gaa   443
Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu
    115                 120                 125

tgc aga cca aag aaa gat aga gca aga caa gaa aat ccc tgt ggg cct   491
Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly Pro
130                 135                 140                 145

tgc tca gag cgg aga aag cat ttg ttt gta caa gat ccg cag acg tgt   539
Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys
                150                 155                 160


aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag ctt   587
Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu
            165                 170                 175

gag tta aac gaa cgt act tgc aga tgt gac aag ccg agg cgg           629
Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
        180                 185                 190

tgagccgggc aggaggaagg agcctccctc agggtttcgg gaaccagatc tctcaccagg 689

aaagactgat acagaacgat cgatacagaa accacgctgc cgccaccaca ccatcaccat 749

cgacagaaca gtccttaatc cagaaacctg aaatgaagga agaggagact ctgcgcagag 809

cactttgggt ccggagggcg agactccggc ggaagcattc ccgggcgggt gacccagcac 869

ggtccctctt ggaattggat tcgccatttt atttttcttg ctgctaaatc accgagcccg 929

gaagattaga gagttttatt tctgggattc ctgtagacac accgcggccg ccagcacact 989

g                                                                 990


<210> 12
<211> 191
<212> PRT
<213> Homo sapiens

<400> 12
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1               5                  10                  15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
            20                  25                  30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
        35                  40                  45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
    50                  55                  60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65                  70                  75                  80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
                85                  90                  95
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Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
          100                 105                 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
        115                 120                 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
    130                 135                 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145                 150                 155                 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
            165                 170                 175


Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
            180                 185                 190

<210> 13
<211> 1997
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (352)..(1608)

<400> 13
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ctcgcttcac ctcgcgggct ccgaatgcgg ggagctcgga tgtccggttt cctgtgaggc 120

ttttacctga cacccgccgc ctttccccgg cactggctgg gagggcgccc tgcaaagttg 180

ggaacgcgga gccccggacc cgctcccgcc gcctccggct cgcccagggg gggtcgccgg 240

gaggagcccg ggggagaggg accaggaggg gcccgcggcc tcgcaggggc gcccgcgccc 300

ccacccctgc ccccgccagc ggaccggtcc cccacccccg gtccttccac c atg cac  357
                                                      Met His
                                                        1

ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg   405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
          5                  10                  15

ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc   453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
     20                  25                  30

gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct   501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
 35                  40                  45                  50

tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta   549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
                 55                  60                  65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag   597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
             70                  75                  80
```

```
tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac   645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
         85                  90                  95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat   693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
    100                 105                 110

aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa   741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
115                 120                 125                 130

tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc   789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
                135                 140                 145

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt   837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
            150                 155                 160

ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg   885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
        165                 170                 175

agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa   933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
    180                 185                 190

ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga   981
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg
195                 200                 205                 210

tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga  1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg
                215                 220                 225

cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc  1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr
            230                 235                 240

tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct  1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala
        245                 250                 255

cag gaa gat ttt atg ttt tcc tcg gat gct gga gat gac tca aca gat  1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp
    260                 265                 270

gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc  1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr
275                 280                 285                 290

tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc  1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro
                295                 300                 305

cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa  1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys
            310                 315                 320

ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca  1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr
        325                 330                 335
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tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat   1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn
    340                 345                 350

cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg   1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu
355                 360                 365                 370

tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg   1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg
                375                 380                 385

cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt   1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser
            390                 395                 400

gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg   1605
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met
        405                 410                 415

agc taagattgta ctgttttcca gttcatcgat tttctattat ggaaaactgt       1658
Ser

gttgccacag tagaactgtc tgtgaacaga gagacccttg tgggtccatg ctaacaaaga 1718

caaaagtctg tctttcctga accatgtgga taactttaca gaaatggact ggagctcatc 1778

tgcaaaaggc ctcttgtaaa gactggtttt ctgccaatga ccaaacagcc aagattttcc 1838

tcttgtgatt tctttaaaag aatgactata taatttattt ccactaaaaa tattgtttct 1898

gcattcattt ttatagcaac aacaattggt aaaactcact gtgatcaata tttttatatc 1958

atgcaaaata tgtttaaaat aaaatgaaaa ttgtattat                        1997
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<210> 14
<211> 419
<212> PRT
<213> Homo sapiens

<400> 14

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Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
  1               5                  10                  15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
            20                  25                  30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
        35                  40                  45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
    50                  55                  60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65                  70                  75                  80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
                85                  90                  95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
            100                 105                 110
```

```
His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
        115                 120                 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
    130                 135                 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145                 150                 155                 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
                165                 170                 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
            180                 185                 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
        195                 200                 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
    210                 215                 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225                 230                 235                 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
                245                 250                 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
            260                 265                 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
        275                 280                 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
    290                 295                 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305                 310                 315                 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
                325                 330                 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
            340                 345                 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
        355                 360                 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
    370                 375                 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385                 390                 395                 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
                405                 410                 415

Gln Met Ser
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<210> 15
<211> 1645
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (322)..(768)

<400> 15
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tccccgggac ccgcctgccc ctcggcgccc cgccccgccg ggccgctccc cgtcgggttc 120

cccagccaca gccttaccta cgggctcctg actccgcaag gcttccagaa gatgctcgaa 180

ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagcccccca ctcagctctt 240

ctcctcctgt gccaggggct ccccgggggа tgagcatggt ggttttccct cggagccccc 300

tggctcggga cgtctgagaa g atg ccg gtc atg agg ctg ttc cct tgc ttc 351
Met Pro Val Met Arg Leu Phe Pro Cys Phe
1 5 10

ctg cag ctc ctg gcc ggg ctg gcg ctg cct gct gtg ccc ccc cag cag 399
Leu Gln Leu Leu Ala Gly Leu Ala Leu Pro Ala Val Pro Pro Gln Gln
15 20 25

tgg gcc ttg tct gct ggg aac ggc tcg tca gag gtg gaa gtg gta ccc 447
Trp Ala Leu Ser Ala Gly Asn Gly Ser Ser Glu Val Glu Val Val Pro
30 35 40

ttc cag gaa gtg tgg ggc cgc agc tac tgc cgg gcg ctg gag agg ctg 495
Phe Gln Glu Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu
45 50 55

gtg gac gtc gtg tcc gag tac ccc agc gag gtg gag cac atg ttc agc 543
Val Asp Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser
60 65 70

cca tcc tgt gtc tcc ctg ctg cgc tgc acc ggc tgc tgc ggc gat gag 591
Pro Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu
75 80 85 90

aat ctg cac tgt gtg ccg gtg gag acg gcc aat gtc acc atg cag ctc 639
Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln Leu
95 100 105

cta aag atc cgt tct ggg gac cgg ccc tcc tac gtg gag ctg acg ttc 687
Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe
110 115 120

tct cag cac gtt cgc tgc gaa tgc cgg cct ctg cgg gag aag atg aag 735
Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu Lys Met Lys
125 130 135

ccg gaa agg tgc ggc gat gct gtt ccc cgg agg taacccaccc cttggaggag 788
Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg
140 145

agagaccccg cacccggctc gtgtatttat taccgtcaca ctcttcagtg actcctgctg 848

gtacctgccc tctatttatt agccaactgt ttccctgctg aatgcctcgc tcccttcaag 908

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acgaggggca gggaaggaca ggaccctcag gaattcagtg ccttcaacaa cgtgagagaa 968

agagagaagc cagccacaga cccctgggag cttccgcttt gaaagaagca agacacgtgg 1028

cctcgtgagg ggcaagctag gccccagagg ccctggaggt ctccaggggc ctgcagaagg 1088

aaagaagggg gccctgctac ctgttcttgg gcctcaggct ctgcacagac aagcagccct 1148

tgctttcgga gctcctgtcc aaagtaggga tgcggattct gctggggccg ccacggcctg 1208

gtggtgggaa ggccggcagc gggcggaggg gattcagcca cttccccctc ttcttctgaa 1268

gatcagaaca ttcagctctg gagaacagtg gttgcctggg ggcttttgcc actccttgtc 1328

ccccgtgatc tcccctcaca ctttgccatt tgcttgtact gggacattgt tctttccggc 1388

cgaggtgcca ccaccctgcc cccactaaga gacacataca gagtgggccc cgggctggag 1448

aaagagctgc ctggatgaga aacagctcag ccagtgggga tgaggtcacc aggggaggag 1508

cctgtgcgtc ccagctgaag gcagtggcag gggagcaggt tccccaaggg ccctggcacc 1568

cccacaagct gtccctgcag ggccatctga ctgccaagcc agattctctt gaataaagta 1628

ttctagtgtg gaaacgc                                                 1645
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<210> 16
<211> 149
<212> PRT
<213> Homo sapiens

<400> 16

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Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
  1               5                  10                  15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
            20                  25                  30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
        35                  40                  45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
    50                  55                  60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65                  70                  75                  80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
                85                  90                  95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
            100                 105                 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
        115                 120                 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp
    130                 135                 140

Ala Val Pro Arg Arg
145
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<210> 17
<211> 2029
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (411)..(1472)

<400> 17
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aactagaacc tgcggcatac attggagaga ttttttttaat tttctggaca tgaagtaaat 120

ttagagtgct ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa 180

cattttgatt tttttcatct ctctctcccc acccctaaga ttgtgcaaaa aaagcgtacc 240

ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg 300

tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360

gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416
Met Tyr
1

aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg 464
Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
5 10 15

gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag 512
Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln
20 25 30

tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg 560
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
35 40 45 50

gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga 608
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
55 60 65

tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca 656
Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala
70 75 80

tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca 704
Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr
85 90 95

cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga 752
Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
100 105 110

gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca 800
Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr
115 120 125 130

ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc 848
Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys
135 140 145

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aat gaa gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc   896
Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser
            150                 155                 160

aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta   944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu
        165                 170                 175

gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca   992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr
    180                 185                 190

gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct   1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro
195                 200                 205                 210

gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg   1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met
                215                 220                 225

cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca   1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro
            230                 235                 240

ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt   1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys
        245                 250                 255

ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa   1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys
    260                 265                 270

aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc   1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys
275                 280                 285                 290

ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta   1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu
                295                 300                 305

ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc   1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr
            310                 315                 320

aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt   1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe
        325                 330                 335

cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct   1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro
    340                 345                 350

tgattcagcg ttccaagttc cccatccctg tcatttttaa cagcatgctg ctttgccaag 1532

ttgctgtcac tgttttttc ccaggtgtta aaaaaaaaat ccattttaca cagcaccaca 1592

gtgaatccag accaaccttc cattcacacc agctaaggag tccctggttc attgatggat 1652

gtcttctagc tgcagatgcc tctgcgcacc aaggaatgga gaggagggga cccatgtaat 1712

ccttttgttt agttttgttt ttgtttttg gtgaatgaga aaggtgtgct ggtcatggaa 1772

tggcaggtgt catatgactg attactcaga gcagatgagg aaaactgtag tctctgagtc 1832
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ctttgctaat cgcaactctt gtgaattatt ctgattcttt tttatgcaga atttgattcg 1892

tatgatcagt actgactttc tgattactgt ccagcttata gtcttccagt ttaatgaact 1952

accatctgat gtttcatatt taagtgtatt taaagaaaat aaacaccatt attcaagcca 2012

aaaaaaaaaa aaaaaaa 2029

<210> 18
<211> 354
<212> PRT
<213> Homo sapiens

<400> 18

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Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
  1               5                  10                  15

Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
            20                  25                  30

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
         35                  40                  45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
     50                  55                  60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
 65                  70                  75                  80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
                85                  90                  95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
            100                 105                 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
        115                 120                 125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
    130                 135                 140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145                 150                 155                 160

Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
                165                 170                 175

Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
            180                 185                 190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
        195                 200                 205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
    210                 215                 220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
225                 230                 235                 240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
                245                 250                 255
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Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
            260                 265                 270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
        275                 280                 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
    290                 295                 300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
305                 310                 315                 320

His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
                325                 330                 335

Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
            340                 345                 350

Asn Pro
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<210> 19
<211> 1830
<212> DNA
<213> Orf virus

<220>
<221> CDS
<222> (312)..(755)

<400> 19

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cggccacgcg gccgcgaact gcgcgctcgc gcgcgtggcg accgcgctga cgcgccgcgt 60

gcccgcgagc cggcacggcc tcgcggaggg cggcacgccg ccgtggacgc tgctgctggc 120

ggtggccgcg gtggcggtgc tcggcgtggt ggcaatttcg ctgctgcgcc gcgcgctaag 180

aatacggttt agatactcaa agtctatcca gacacttaga gtgtaacttt gagtaaaaaa 240

tgtaaatact aacgccaaaa tttcgatagt tgttaagcaa tatataacat ttttaaaacg 300

tcatcaccag c atg aag tta aca gct acg tta caa gtt gtt gtt gca ttg  350
             Met Lys Leu Thr Ala Thr Leu Gln Val Val Val Ala Leu
               1               5                  10

tta ata tgt atg tat aat ttg cca gaa tgc gtg tct cag agt aat gat   398
Leu Ile Cys Met Tyr Asn Leu Pro Glu Cys Val Ser Gln Ser Asn Asp
     15                  20                  25

tca cct cct tca acc aat gac tgg atg cgt aca cta gac aaa agt ggt   446
Ser Pro Pro Ser Thr Asn Asp Trp Met Arg Thr Leu Asp Lys Ser Gly
 30                  35                  40                  45

tgt aaa cct aga gat act gtt gtt tat ttg gga gaa gaa tat cca gaa   494
Cys Lys Pro Arg Asp Thr Val Val Tyr Leu Gly Glu Glu Tyr Pro Glu
                 50                  55                  60

agc act aac cta caa tat aat ccc cgg tgc gta act gtt aaa cga tgc   542
Ser Thr Asn Leu Gln Tyr Asn Pro Arg Cys Val Thr Val Lys Arg Cys
             65                  70                  75

agt ggt tgc tgt aac ggt gac ggt caa ata tgt aca gcg gtt gaa aca   590
Ser Gly Cys Cys Asn Gly Asp Gly Gln Ile Cys Thr Ala Val Glu Thr
         80                  85                  90
```

```
aga aat aca act gta aca gtt tca gta acc ggc gtg tct agt tcg tct   638
Arg Asn Thr Thr Val Thr Val Ser Val Thr Gly Val Ser Ser Ser Ser
     95                  100                 105

ggt act aat agt ggt gta tct act aac ctt caa aga ata agt gtt aca   686
Gly Thr Asn Ser Gly Val Ser Thr Asn Leu Gln Arg Ile Ser Val Thr
110                 115                 120                 125

gaa cac aca aag tgc gat tgt att ggt aga aca acg aca aca cct acg   734
Glu His Thr Lys Cys Asp Cys Ile Gly Arg Thr Thr Thr Thr Pro Thr
                130                 135                 140

acc act agg gaa cct aga cga taactaataa caaaaaatgt ttatttttgt      785
Thr Thr Arg Glu Pro Arg Arg
            145

aaatacttaa ttattacaca ctttacaata atctcaaaaa taaattgcgt gcccggacgg 845

ctgcagctgg tgacgctgct gtgtcacaca ctgcgtattc gattcaagtt cactaacgcc 905

actaaactag ttgtgcgtgt ccgagtgtta accgtacgtc aaactaacat cttacctgtc 965

cgtgacaaga actaaaactt gaaccacata tttttaaagt atatttaaca aaatcactca 1025

cactcacaca atcataaaca ccacaaccac aaccaaacac gcatgagaat taatattctt 1085

acttatccgt aacactctat gctgtacatc aacgcatcag agcagtctga gtctgactaa 1145

tggcggcaaa cgggaacgca ggcgcgacat aatcactgag aatctccgca gcaaccgctc 1205

aaggacatct ctagcgctaa cggctgtttg tcattccccc gtgtgttcat ctcacacgac 1265

attgtgaccg tcgcaaagca cacattcaaa gtgccgcatg tggaagaatt caccgtcgag 1325

acacacacca taattaaaca agatcagtgc ataagagaga ttagcattct acagcacacc 1385

acgtgcgaat acggacctcg taattgttta gactagaaca cctctggtct aaacaacatg 1445

tccgatctta gaacagagtt tatgacgcat atgtaactgt gttctttatg tagaagttat 1505

cttttatgtc actcccttgt cttagatgag ttatacatga catgatgtat gtgtcgcccg 1565

cggcggcgcg gggcgctcgg cggcggggct gctgcgcgcg gcgggcccgc ggtggcggcg 1625

gctggcgcgg cgctgcggcc gcgggcgcgc ggcggggtag cggcccgccc gcccgggcgc 1685

ccgccgcagc ccttgccccg gaccaggcgc cacggagcaa agtgaaaaag gaccgcctag 1745

cagtcgagac cctcccgccg cagccgcgac accccacacc cgccttccac ccgccagacg 1805

ccaacaccac agccaacaag catgc                                       1830
```

<210> 20
<211> 148
<212> PRT
<213> Orf virus

<400> 20

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Met Lys Leu Thr Ala Thr Leu Gln Val Val Val Ala Leu Leu Ile Cys
  1               5                  10                  15
```

```
Met Tyr Asn Leu Pro Glu Cys Val Ser Gln Ser Asn Asp Ser Pro Pro
            20                  25                  30

Ser Thr Asn Asp Trp Met Arg Thr Leu Asp Lys Ser Gly Cys Lys Pro
        35                  40                  45

Arg Asp Thr Val Val Tyr Leu Gly Glu Glu Tyr Pro Glu Ser Thr Asn
    50                  55                  60

Leu Gln Tyr Asn Pro Arg Cys Val Thr Val Lys Arg Cys Ser Gly Cys
65                  70                  75                  80

Cys Asn Gly Asp Gly Gln Ile Cys Thr Ala Val Glu Thr Arg Asn Thr
                85                  90                  95

Thr Val Thr Val Ser Val Thr Gly Val Ser Ser Ser Ser Gly Thr Asn
            100                 105                 110


Ser Gly Val Ser Thr Asn Leu Gln Arg Ile Ser Val Thr Glu His Thr
        115                 120                 125

Lys Cys Asp Cys Ile Gly Arg Thr Thr Thr Thr Pro Thr Thr Thr Arg
    130                 135                 140

Glu Pro Arg Arg
145


<210> 21
<211> 851
<212> DNA
<213> Orf virus

<220>
<221> CDS
<222> (2)..(223)

<400> 21
c ggc cac gcg gcc gcg aac tgc gcg ctc gcg cgc gtg gcg acc gcg ctg 49
  Gly His Ala Ala Ala Asn Cys Ala Leu Ala Arg Val Ala Thr Ala Leu
    1               5                   10                  15

acg cgc cgc gtg ccc gcg agc cgg cac ggc ctc gcg gag ggc ggc acg   97
Thr Arg Arg Val Pro Ala Ser Arg His Gly Leu Ala Glu Gly Gly Thr
            20                  25                  30

ccg ccg tgg acg ctg ctg ctg gcg gtg gcc gcg gtg acg gtg ctc ggc   145
Pro Pro Trp Thr Leu Leu Leu Ala Val Ala Ala Val Thr Val Leu Gly
        35                  40                  45

gtg gtg gcg gtt tca ctg ctg cgg cgc gcg ctg cgg gta cgc tac cgc   193
Val Val Ala Val Ser Leu Leu Arg Arg Ala Leu Arg Val Arg Tyr Arg
    50                  55                  60

ttc gcg cgg ccg gcc gcg ctg cgc gcg tag ccgcgcaaaa tgtaaattat     243
Phe Ala Arg Pro Ala Ala Leu Arg Ala
65                  70

aacgcccaac ttttaagggt gaggcgccat gaagttgctc gtcggcatac tagtagccgt 303

gtgcttgcac cagtatctgc tgaacgcgga cagcaacacg aaaggatggt ccgaagtgct 363
```

gaaaggcagc gagtgcaagc ctaggccgat tgttgttcct gtaagcgaga cgcacccaga 423

gctgacttct cagcggttca acccgccgtg tgtcacgttg atgcgatgcg gcgggtgctg 483

caacgacgag agcttggaat gcgtccccac ggaagaagta aacgtgagca tggaactcct 543

gggggcgtcg ggctccggta gtaacgggat gcaacgtctg agcttcgtag agcataagaa 603

atgcgattgt agaccacgat tcacaaccac gccaccgacg accacaaggc cgcccagaag 663

acgccgctag aacttttat ggaccgcaga tccaaacgat ggatgcgatc aggtacatgc 723

ggaagaaggc gccacggagc aaagtgaaaa aggaccgcct agcagtcgag accctcccgc 783

cgcagccgcg gacaccccac acccgccttc cacccgccag acgccaacac cgcagccaac 843

aagcatgc 851

<210> 22
<211> 73
<212> PRT
<213> Orf virus

<400> 22

Gly	His	Ala	Ala	Ala	Asn	Cys	Ala	Leu	Ala	Arg	Val	Ala	Thr	Ala	Leu
1				5				10					15		
Thr	Arg	Arg	Val	Pro	Ala	Ser	Arg	His	Gly	Leu	Ala	Glu	Gly	Gly	Thr
		20					25					30			
Pro	Pro	Trp	Thr	Leu	Leu	Leu	Ala	Val	Ala	Ala	Val	Thr	Val	Leu	Gly
	35					40					45				
Val	Val	Ala	Val	Ser	Leu	Leu	Arg	Arg	Ala	Leu	Arg	Val	Arg	Tyr	Arg
50					55					60					
Phe	Ala	Arg	Pro	Ala	Ala	Leu	Arg	Ala							
65					70										

<210> 23
<211> 2305
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (404)..(991)

<400> 23
ttcttggggc tgatgtccgc aaatatgcag aattaccggc cgggtcgctc ctgaagccag 60

cgcggggagc gagcgcggcg gcggccagca ccgggaacgc accgaggaag aagcccagcc 120

cccgccctcc gcccccttccg tccccacccc ctacccggcg gcccaggagg ctccccggct 180

gcggcgcgca ctccctgttt ctcctcctcc tggctggcgc tgcctgcctc tccgcactca 240

ctgctcgccg ggcgccgtcc gccagctccg tgctccccgc gccaccctcc tccgggccgc 300

```
gctccctaag ggatggtact gaatttcgcc gccacaggag accggctgga gcgcccgccc 360

cgcgcctcgc ctctcctccg agcagccagc gcctcgggac gcg atg agg acc ttg   415
                                              Met Arg Thr Leu
                                                1

gct tgc ctg ctg ctc ctc ggc tgc gga tac ctc gcc cat gtt ctg gcc   463
Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala His Val Leu Ala
  5                  10                  15                  20

gag gaa gcc gag atc ccc cgc gag gtg atc gag agg ctg gcc cgc agt   511
Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg Leu Ala Arg Ser
                 25                  30                  35

cag atc cac agc atc cgg gac ctc cag cga ctc ctg gag ata gac tcc   559
Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu Glu Ile Asp Ser
             40                  45                  50

gta ggg agt gag gat tct ttg gac acc agc ctg aga gct cac ggg gtc   607
Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg Ala His Gly Val
         55                  60                  65

cac gcc act aag cat gtg ccc gag aag cgg ccc ctg ccc att cgg agg   655
His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu Pro Ile Arg Arg
     70                  75                  80

aag aga agc atc gag gaa gct gtc ccc gct gtc tgc aag acc agg acg   703
Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys Lys Thr Arg Thr
 85                  90                  95                 100

gtc att tac gag att cct cgg agt cag gtc gac ccc acg tcc gcc aac   751
Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro Thr Ser Ala Asn
                105                 110                 115

ttc ctg atc tgg ccc ccg tgc gtg gag gtg aaa cgc tgc acc ggc tgc   799
Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg Cys Thr Gly Cys
            120                 125                 130

tgc aac acg agc agt gtc aag tgc cag ccc tcc cgc gtc cac cac cgc   847
Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg Val His His Arg
        135                 140                 145

agc gtc aag gtg gcc aag gtg gaa tac gtc agg aag aag cca aaa tta   895
Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys Lys Pro Lys Leu
    150                 155                 160

aaa gaa gtc cag gtg agg tta gag gag cat ttg gag tgc gcc tgc gcg   943
Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu Cys Ala Cys Ala
165                 170                 175                 180

acc aca agc ctg aat ccg gat tat cgg gaa gag gac acg gat gtg agg   991
Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp Thr Asp Val Arg
                185                 190                 195

tgaggatgag ccgcagccct ttcctgggac atggatgtac atggcgtgtt acattcctga 1051

acctactatg tacggtgctt tattgccagt gtgcggtctt tgttctcctc cgtgaaaaac 1111

tgtgtccgag aacactcggg agaacaaaga gacagtgcac atttgtttaa tgtgacatca 1171

aagcaagtat tgtagcactc ggtgaagcag taagaagctt ccttgtcaaa aagagagaga 1231
```

gagagagaga gagagaaaac aaaaccacaa atgacaaaaa caaaacggac tcacaaaaat 1291

atctaaactc gatgagatgg agggtcgccc cgtgggatgg aagtgcagag gtctcagcag 1351

actggatttc tgtccgggtg gtcacaggtg ctttttgcc gaggatgcag agcctgcttt 1411

gggaacgact ccagaggggt gctggtgggc tctgcagggc ccgcaggaag caggaatgtc 1471

ttggaaaccg ccacgcgaac tttagaaacc acacctcctc gctgtagtat ttaagcccat 1531

acagaaacct tcctgagagc cttaagtggt ttttttttt gtttttgttt tgttttttt 1591

ttttttgttt ttttttttt ttttttttt tacaccataa agtgattatt aagcttcctt 1651

ttactctttg gctagctttt ttttttttt ttttttttt ttttttaat tatctcttgg 1711

atgacattta caccgataac acacaggctg ctgtaactgt caggacagtg cgacggtatt 1771

tttcctagca agatgcaaac taatgagatg tattaaaata aacatggtat acctacctat 1831

gcatcatttc ctaaatgttt ctggctttgt gtttctccct taccctgctt tatttgttaa 1891

tttaagccat tttgaaagaa ctatgcgtca accaatcgta cgccgtccct gcggcacctg 1951

ccccagagcc cgtttgtggc tgagtgacaa cttgttcccc gcagtgcaca cctagaatgc 2011

tgtgttccca cgcggcacgt gagatgcatt gccgcttctg tctgtgttgt tggtgtgccc 2071

tggtgccgtg gtggcggtca ctccctctgc tgccagtgtt tggacagaac ccaaattctt 2131

tatttttggt aagatattgt gctttacctg tattaacaga aatgtgtgtg tgtggtttgt 2191

ttttttgtaa aggtgaagtt tgtatgttta cctaatatta cctgttttgt atacctgaga 2251

gcctgctatg ttcttctttt gttgatccaa aattaaaaaa aaaataccac caac 2305

<210> 24
<211> 196
<212> PRT
<213> Homo sapiens

<400> 24

Met	Arg	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Leu	Gly	Cys	Gly	Tyr	Leu	Ala
1				5				10					15		
His	Val	Leu	Ala	Glu	Glu	Ala	Glu	Ile	Pro	Arg	Glu	Val	Ile	Glu	Arg
			20					25					30		
Leu	Ala	Arg	Ser	Gln	Ile	His	Ser	Ile	Arg	Asp	Leu	Gln	Arg	Leu	Leu
		35					40					45			
Glu	Ile	Asp	Ser	Val	Gly	Ser	Glu	Asp	Ser	Leu	Asp	Thr	Ser	Leu	Arg
	50					55					60				
Ala	His	Gly	Val	His	Ala	Thr	Lys	His	Val	Pro	Glu	Lys	Arg	Pro	Leu
65					70					75					80
Pro	Ile	Arg	Arg	Lys	Arg	Ser	Ile	Glu	Glu	Ala	Val	Pro	Ala	Val	Cys
				85					90					95	
Lys	Thr	Arg	Thr	Val	Ile	Tyr	Glu	Ile	Pro	Arg	Ser	Gln	Val	Asp	Pro
			100					105					110		

```
Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
        115                 120                 125

Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
    130                 135                 140

Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
145                 150                 155                 160

Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
                165                 170                 175

Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
            180                 185                 190

Thr Asp Val Arg
        195
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<210> 25
<211> 2137
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (983)..(1705)

<400> 25
ccctgcctgc ctccctgcgc acccgcagcc tcccccgctg cctccctagg gctcccctcc 60

ggccgccagc gcccattttt cattccctag atagagatac tttgcgcgca cacacataca 120

tacgcgcgca aaaaggaaaa aaaaaaaaaa aagcccaccc tccagcctcg ctgcaaagag 180

aaaaccggag cagccgcagc tcgcagctcg cagcccgcag cccgcagagg acgcccagag 240

cggcgagcgg gcgggcagac ggaccgacgg actcgcgccg cgtccacctg tcggccgggc 300

ccagccgagc gcgcagcggg cacgccgcgc gcgcggagca gccgtgcccg ccgcccgggc 360

ccgccgccag ggcgcacacg ctcccgcccc cctacccggc ccgggcggga gtttgcacct 420

ctccctgccc gggtgctcga gctgccgttg caaagccaac tttggaaaaa gtttttgggg 480

ggagacttgg gccttgaggt gcccagctcc gcgctttccg attttggggg cctttccaga 540

aaatgttgca aaaaagctaa gccggcgggc agaggaaaac gcctgtagcc ggcgagtgaa 600

gacgaaccat cgactgccgt gttccttttc ctcttggagg ttggagtccc ctgggcgccc 660

ccacacggct agacgcctcg gctggttcgc gacgcagccc cccggccgtg gatgctgcac 720

tcgggctcgg gatccgccca ggtagcggcc tcggacccag gtcctgcgcc caggtcctcc 780

cctgcccccc agcgacggag ccggggccgg gggcggcggc gccgggggca tgcgggtgag 840

ccgcggctgc agaggcctga gcgcctgatc gccgcggacc cgagccgagc ccacccccct 900

ccccagcccc ccaccctggc cgcgggggcg gcgcgctcga tctacgcgtt cggggccccg 960

```
cggggccggg cccggagtcg gc atg aat cgc tgc tgg gcg ctc ttc ctg tct  1012
                          Met Asn Arg Cys Trp Ala Leu Phe Leu Ser
                            1               5                  10

ctc tgc tgc tac ctg cgt ctg gtc agc gcc gag ggg gac ccc att ccc  1060
Leu Cys Cys Tyr Leu Arg Leu Val Ser Ala Glu Gly Asp Pro Ile Pro
                 15                  20                  25

gag gag ctt tat gag atg ctg agt gac cac tcg atc cgc tcc ttt gat  1108
Glu Glu Leu Tyr Glu Met Leu Ser Asp His Ser Ile Arg Ser Phe Asp
             30                  35                  40

gat ctc caa cgc ctg ctg cac gga gac ccc gga gag gaa gat ggg gcc  1156
Asp Leu Gln Arg Leu Leu His Gly Asp Pro Gly Glu Glu Asp Gly Ala
         45                  50                  55


gag ttg gac ctg aac atg acc cgc tcc cac tct gga ggc gag ctg gag  1204
Glu Leu Asp Leu Asn Met Thr Arg Ser His Ser Gly Gly Glu Leu Glu
     60                  65                  70

agc ttg gct cgt gga aga agg agc ctg ggt tcc ctg acc att gct gag  1252
Ser Leu Ala Arg Gly Arg Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu
 75                  80                  85                  90

ccg gcc atg atc gcc gag tgc aag acg cgc acc gag gtg ttc gag atc  1300
Pro Ala Met Ile Ala Glu Cys Lys Thr Arg Thr Glu Val Phe Glu Ile
                 95                 100                 105

tcc cgg cgc ctc ata gac cgc acc aac gcc aac ttc ctg gtg tgg ccg  1348
Ser Arg Arg Leu Ile Asp Arg Thr Asn Ala Asn Phe Leu Val Trp Pro
            110                 115                 120

ccc tgt gtg gag gtg cag cgc tgc tcc ggc tgc tgc aac aac cgc aac  1396
Pro Cys Val Glu Val Gln Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn
        125                 130                 135

gtg cag tgc cgc ccc acc cag gtg cag ctg cga cct gtc cag gtg aga  1444
Val Gln Cys Arg Pro Thr Gln Val Gln Leu Arg Pro Val Gln Val Arg
    140                 145                 150

aag atc gag att gtg cgg aag aag cca atc ttt aag aag gcc acg gtg  1492
Lys Ile Glu Ile Val Arg Lys Lys Pro Ile Phe Lys Lys Ala Thr Val
155                 160                 165                 170

acg ctg gaa gac cac ctg gca tgc aag tgt gag aca gtg gca gct gca  1540
Thr Leu Glu Asp His Leu Ala Cys Lys Cys Glu Thr Val Ala Ala Ala
                175                 180                 185

cgg cct gtg acc cga agc ccg ggg ggt tcc cag gag cag cga gcc aaa  1588
Arg Pro Val Thr Arg Ser Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys
            190                 195                 200

acg ccc caa act cgg gtg acc att cgg acg gtg cga gtc cgc cgg ccc  1636
Thr Pro Gln Thr Arg Val Thr Ile Arg Thr Val Arg Val Arg Arg Pro
        205                 210                 215

ccc aag ggc aag cac cgg aaa ttc aag cac acg cat gac aag acg gca  1684
Pro Lys Gly Lys His Arg Lys Phe Lys His Thr His Asp Lys Thr Ala
    220                 225                 230
```

```
ctg aag gag acc ctt gga gcc taggggcatc ggcaggagag tgtgtgggca      1735
Leu Lys Glu Thr Leu Gly Ala
235                 240

gggttattta atatggtatt tgctgtattg cccccatggg gccttggagt agataatatt 1795

gtttccctcg tccgtctgtc tcgatgcctg attcggacgg ccaatggtgc ctcccccacc 1855

cctccacgtg tccgtccacc cttccatcag cgggtctcct cccagcggcc tccggctctt 1915

gcccagcagc tcaagaagaa aaagaaggac tgaactccat cgccatcttc ttcccttaac 1975

tccaagaact tgggataaga gtgtgagaga gactgatggg gtcgctcttt gggggaaacg 2035

ggttccttcc cctgcacctg gcctgggcca cacctgagcg ctgtggactg tcctgaggag 2095

ccctgaggac ctctcagcat agcctgcctg atccctgaac cc                    2137
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<210> 26
<211> 241
<212> PRT
<213> Homo sapiens

<400> 26

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Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
  1               5                  10                  15

Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
             20                  25                  30

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
         35                  40                  45

His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
     50                  55                  60

Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
 65                  70                  75                  80

Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
                 85                  90                  95

Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
            100                 105                 110

Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
        115                 120                 125

Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
    130                 135                 140

Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
145                 150                 155                 160

Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
                165                 170                 175

Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
            180                 185                 190

Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
        195                 200                 205
```

```
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
    210                 215                 220

Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
225                 230                 235                 240

Ala
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<210> 27
<211> 3007
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (492)..(1529)

<400> 27

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gcccggagag ccgcatctat tggcagcttt gttattgatc agaaactgct cgccgccgac 60

ttggcttcca gtctggctgc gggcaaccct tgagttttcg cctctgtcct gtcccccgaa 120

ctgacaggtg ctcccagcaa cttgctgggg acttctcgcc gctccccccgc gtccccaccc 180

cctcattcct ccctcgcctt caccccccacc cccaccactt cgccacagct caggatttgt 240

ttaaaccttg ggaaactggt tcaggtccag gttttgcttt gatccttttc aaaaactgga 300

gacacagaag agggctctag gaaaaagttt tggatgggat tatgtggaaa ctaccctgcg 360

attctctgct gccagagcag gctcggcgct tccacccccag tgcagccttc ccctggcggt 420

ggtgaaagag actcgggagt cgctgcttcc aaagtgcccg ccgtgagtga gctctcaccc 480

cagtcagcca a atg agc ctc ttc ggg ctt ctc ctg ctg aca tct gcc ctg  530
             Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu
               1               5                  10

gcc ggc cag aga cag ggg act cag gcg gaa tcc aac ctg agt agt aaa   578
Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys
     15                  20                  25

ttc cag ttt tcc agc aac aag gaa cag aac gga gta caa gat cct cag   626
Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln
 30                  35                  40                  45

cat gag aga att att act gtg tct act aat gga agt att cac agc cca   674
His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro
                 50                  55                  60

agg ttt cct cat act tat cca aga aat acg gtc ttg gta tgg aga tta   722
Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu
             65                  70                  75

gta gca gta gag gaa aat gta tgg ata caa ctt acg ttt gat gaa aga   770
Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg
         80                  85                  90

ttt ggg ctt gaa gac cca gaa gat gac ata tgc aag tat gat ttt gta   818
Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val
     95                  100                 105
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gaa gtt gag gaa ccc agt gat gga act ata tta ggg cgc tgg tgt ggt   866
Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly
110                 115                 120                 125

tct ggt act gta cca gga aaa cag att tct aaa gga aat caa att agg   914
Ser Gly Thr Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg
                130                 135                 140

ata aga ttt gta tct gat gaa tat ttt cct tct gaa cca ggg ttc tgc   962
Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys
            145                 150                 155

atc cac tac aac att gtc atg cca caa ttc aca gaa gct gtg agt cct   1010
Ile His Tyr Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro
        160                 165                 170

tca gtg cta ccc cct tca gct ttg cca ctg gac ctg ctt aat aat gct   1058
Ser Val Leu Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala
    175                 180                 185

ata act gcc ttt agt acc ttg gaa gac ctt att cga tat ctt gaa cca   1106
Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro
190                 195                 200                 205


gag aga tgg cag ttg gac tta gaa gat cta tat agg cca act tgg caa   1154
Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln
                210                 215                 220

ctt ctt ggc aag gct ttt gtt ttt gga aga aaa tcc aga gtg gtg gat   1202
Leu Leu Gly Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp
            225                 230                 235

ctg aac ctt cta aca gag gag gta aga tta tac agc tgc aca cct cgt   1250
Leu Asn Leu Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg
        240                 245                 250

aac ttc tca gtg tcc ata agg gaa gaa cta aag aga acc gat acc att   1298
Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile
    255                 260                 265

ttc tgg cca ggt tgt ctc ctg gtt aaa cgc tgt ggt ggg aac tgt gcc   1346
Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala
270                 275                 280                 285

tgt tgt ctc cac aat tgc aat gaa tgt caa tgt gtc cca agc aaa gtt   1394
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val
                290                 295                 300

act aaa aaa tac cac gag gtc ctt cag ttg aga cca aag acc ggt gtc   1442
Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val
            305                 310                 315

agg gga ttg cac aaa tca ctc acc gac gtg gcc ctg gag cac cat gag   1490
Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu
        320                 325                 330

gag tgt gac tgt gtg tgc aga ggg agc aca gga gga tag ccgcatcacc    1539
Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly
    335                 340                 345
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accagcagct cttgcccaga gctgtgcagt gcagtggctg attctattag agaacgtatg 1599

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Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
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Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
         35                  40                  45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
     50                  55                  60

His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
 65                  70                  75                  80

Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
                 85                  90                  95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
            100                 105                 110


Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
        115                 120                 125

Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
    130                 135                 140

Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                 150                 155                 160

Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
                165                 170                 175

Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
            180                 185                 190

Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
        195                 200                 205

Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
    210                 215                 220

Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225                 230                 235                 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
                245                 250                 255

Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
            260                 265                 270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
        275                 280                 285

His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
    290                 295                 300

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
305                 310                 315                 320

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Cys Val Cys Arg Gly Ser Thr Gly Gly
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ctg ctg aac gcg gac agc acg aaa aca tgg tcc gaa gtg ttt gaa aac 96
Leu Leu Asn Ala Asp Ser Thr Lys Thr Trp Ser Glu Val Phe Glu Asn
20 25 30

agc ggg tgc aag cca agg ccg atg gtc ttt cga gta cac gac gag cac 144
Ser Gly Cys Lys Pro Arg Pro Met Val Phe Arg Val His Asp Glu His
35 40 45

ccg gag cta act tct cag cgg ttc aac ccg ccg tgt gtc acg ttg atg 192
Pro Glu Leu Thr Ser Gln Arg Phe Asn Pro Pro Cys Val Thr Leu Met
50 55 60

cga tgc ggc ggg tgc tgc aac gac gag agc tta gaa tgc gtc ccc acg 240
Arg Cys Gly Gly Cys Cys Asn Asp Glu Ser Leu Glu Cys Val Pro Thr
65 70 75 80

gaa gag gca aac gta acg atg caa ctc atg gga gcg tcg gtc tcc ggt 288
Glu Glu Ala Asn Val Thr Met Gln Leu Met Gly Ala Ser Val Ser Gly
85 90 95

ggt aac ggg atg caa cat ctg agc ttc gta gag cat aag aaa tgc gat 336
Gly Asn Gly Met Gln His Leu Ser Phe Val Glu His Lys Lys Cys Asp
100 105 110

tgt aaa cca cca ctc acg acc acg cca ccg acg acc aca agg ccg ccc 384
Cys Lys Pro Pro Leu Thr Thr Thr Pro Pro Thr Thr Thr Arg Pro Pro
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aga aga cgc cgc tag 399
Arg Arg Arg Arg
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Leu Leu Asn Ala Asp Ser Thr Lys Thr Trp Ser Glu Val Phe Glu Asn
20 25 30

Ser Gly Cys Lys Pro Arg Pro Met Val Phe Arg Val His Asp Glu His
35 40 45

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Pro Glu Leu Thr Ser Gln Arg Phe Asn Pro Pro Cys Val Thr Leu Met
     50                  55                  60

Arg Cys Gly Gly Cys Cys Asn Asp Glu Ser Leu Glu Cys Val Pro Thr
 65                  70                  75                  80

Glu Glu Ala Asn Val Thr Met Gln Leu Met Gly Ala Ser Val Ser Gly
                 85                  90                  95

Gly Asn Gly Met Gln His Leu Ser Phe Val Glu His Lys Lys Cys Asp
            100                 105                 110

Cys Lys Pro Pro Leu Thr Thr Thr Pro Pro Thr Thr Thr Arg Pro Pro
        115                 120                 125

Arg Arg Arg Arg
    130
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